FORM PTO-1390 (REV. 10-94) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER

80541

U.S. APPLICATION NO (If known, see 37 C F R 1:

09/673779

INTERNATIONAL APPLICATION NO. PCT/NL99/00223

INTERNATIONAL FILING DATE
19 April 1999

PRIORITY DATE CLAIMED 20 April 1998

TITLE OF INVENTION

METHOD FOR THE RAPID DETERMINATION OF BACTERIA

APPLICANT(S) FOR DO/EO/US

Gijsbert Johan JANSEN, John Edward DEGENER, and Gjalt Wietze WELLING

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

- 1. \(\times\) This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
- 2.

 This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
- 3. This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
- 4.

 A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
- 5.

 ✓ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. 🕱 is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. \Box has been transmitted by the International Bureau.
 - c. \square is not required, as the application was filed in the United States Receiving Office (RO/US)
- 6. □ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
- 7.

 Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. \square are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. \square have been transmitted by the International Bureau.
 - c. D have not been made; however, the time limit for making such amendments has NOT expired.
 - d. \Box have not been made and will not be made.
- A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
- 9. An oath or declaration of the inventor(s) (35 U.S.C. 371(c)4)). (Unexecuted)
- 10.

 A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5).

Items 11. to 16. below concern document(s) or information included:

- 11.

 An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
- 12. \square An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
- 13.

 A FIRST preliminary amendment.

A SECOND or SUBSEQUENT preliminary amendment.

- 14. \square A substitute specification.
- 15.

 A change of power of attorney and/or address letter.
- 16. □ Other items or information:

I hereby certify that this paper is being deposited with the United States Postal Service as Express Mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. /20231, on this date,

Date

Express Mail Label No. EL215 070873 US

U.S. APPLICATION NO (If known, see 37 C.F.R. 1.5) PCT/NL99/00223			attorney's docket number 80541			
09/0	09/012				PTO USE ONLY	
17. ☑ The following to BASIC NATIONAL Description						
	al preliminary examina					
	No international preliminary examination fee paid to USPTO (37 CFR 1.482), but international search fee paid to USPTO (37 CFR 1.445(a)(2) \$700.00					
	Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$970.00					
		tion fee paid to USPTO CT Article 33(2)-(4) .				
	ENTER A	PPROPRIATE BASIC	FEE AMOUNT =	\$860.00		
Surcharge of \$130.00 from the earliest prior		or declaration later than (e).	n □20 □30 months	\$130.00		
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE			
Total claims	26-20=	6	x \$18.00	\$108.00		
Independent claims	1-3=	0	x \$80.00	\$		
MULTIPLE DEPEND	DENT CLAIM(S) (if ap	pplicable)	+ 270.00	\$		
	TOTAL OF ABOVI	E CALCULATIONS	=	\$990.00		
•	ling by small entity, if te 37 CFR 1.9, 1.27, 1	\$				
		\$				
Processing fee of \$130 months from the earlie		\$				
		TOTAL 1	NATIONAL FEE =	\$990.00		
_	enclosed assignment (3 propriate cover sheet (-	\$			
		TOTAL F	EES ENCLOSED =	\$990.00		
				Amount to be: refunded	\$	
				charged	\$	
 a. ⊠ A check in the amount of \$990.00 to cover the above fees is enclosed. b. □ Please charge my Deposit Account No in the amount of \$ to cover the above fees. A duplicate copy of this sheet is enclosed. c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 23-0920. A duplicate copy of this sheet is enclosed. 						
NOTE. Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.						
send all correspondence WELSH & KATZ, 120 South Riverside 22nd Floor	, LTD. e Plaza	Speklet				
Chicago, Illinois 60606 Telephone: 312/655-1500 Gerald T. Shekleton NAME						

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re U.S. Pa	atent Application)
Applicant:	JANSEN et al.)
Serial No.:	Not Yet Assigned)
Filed:	Herewith)
For:	METHOD FOR THE RAPID DETERMINATION OF BACTERIA)

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents Washington, D.C. 20231

Sir:

This is a Preliminary Amendment for entry in the above-identified application.

In the Specification:

Please add the attached Abstract page.

In the Claims:

Please amend claims as follows:

- 1. A method for determining a bacterium suspected of being present in a sample comprising
- a) testing said sample by Gram-staining and
- b) testing said sample with a probe according to an in situ hybridisation protocol selected on the basis of the outcome of said Gram-staining.
- 2. A method according to claim 1 wherein said sample is a clinical sample.

- 3. A method according to claim 2 wherein said sample is mammalian blood preferably being derived from a human.
- 4. A method according to claim 1[, 2 or 3] wherein said Gram-staining indicates the presence of a Gram-negative bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.
- 5. A method according to claim 4 wherein said character is of the rod type, further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found *Bacherichia colia*, in *Klebsiella pneumoniae*, in *Klebsiella oxytoca*, in *Serratia marcescens*, in *Enterobacter aerogenes*, in *Enterobacter cloacae*, in *Proteus vulgaris*, in *Proteus mirabilis*, in *Salmonella typhi*, in *Pseudomonas aeruginosa*.
- 6. A method according to claim 5 wherein said nucleic acid is ribosomal RNA.
- 7. A method according to claim 6 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GTAGCCCTACTCGTAAGG or GAGCAAAGGTATTAACTTTACTCCC or GTTAGCCGTCCCTTTCTGG.
- 8. A method according to claim 4 wherein said character is of the coccus type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.

- 9. A method according to claim 1[, 2 or 3] wherein said Gram-staining indicates the presence of a Gram-positive bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.
- 10. A method according to claim 9 wherein said character is of the rod type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme and/or Proteinase K.
- 11. a method according to claim 9 wherein said character is of the coccus type, further comprising determining a chain-like or clump-like character of said bacteria.
- 12. A method according to claim 11 wherein said character is chain-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.
- 13. A method according to claim 12 further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in *Enterococcus faecalis*, in *Streptococcus pneumoniae*, in *Streptococcus mitis*, in *Streptococcus viridans*, in *Streptococcus ganguis*, in *Enterococcus faecium*.
- 14. A method according to claim 13 wherein said nucleic acid is ribosomal RNA.

- 15. A method according to claim 14 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence TTATCCCCCTCTGATGGG or AGAGAAGCAAGCTTCTCGTCCG or GCCACTCCTCTTTTCCGG.
- 16. A method according to claim 11 wherein said character is clump-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysotaphin and/or Proteinase K.
- 17. A method according to claim 16 further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in *Staphylococcus aureus*, in *Staphylococcus haemolyticus*, in *Staphylococcus saprophyticus*.
- 18. A method according to claim 17 wherein said nucleic acid is ribosomal RNA.
- 19. A method according to claim 18 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGGCTCTA or AGAGAAGCAAGCTTCTCGTCCGTT.
- 20. A method according to any of claim[s 4 to 19] 4 further comprising hybridising said sample with at least one positive control probe and/or with at least one negative control probe.

- 21. A method according to claim 20 wherein said positive control probe comprising no more than five mismatches with a probe with the sequence GCTGCCTCCCGTAGGAGT and/or wherein said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGGCAGC.
- 22. A method according to anyone of claim[s 1 to 21] 1 further comprising a one-step procedure to bind bacteria present in said sample to a microscopic slide and simultaneously fix intracellular structures.
- 23. A method according to anyone of claim[s 1 to 22] 1 wherein said probe is selected for its reactivity with one or a group of bacterial genera and/or species having congruent susceptibility to antibiotic treatment.
- 24. A probe detecting or identifying a bacterium in a sample, preferably a clinical sample, said probe designed to hybridise specifically with nucleic acid in bacteria with congruent susceptibility or resistance to antibiotics.
- 25. A probe according to claim 24 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GTAGCCCTACTCGTAAGG or GAGCAAAGGTATTAACTTTACTCCC or GTTAGCCGTCCCTTTCTGG or

TTATCCCCCTCTGATGGG or AGAGAAGCAAGCTTCTCGTCCG or GCCACTCCTCTTTTCCGG or GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGCTCTA or AGAGAAGCAAGCTTCTCGTCCGTT.

26. A diagnostic test kit comprising means for detecting or identifying a bacterium suspected of being present in a sample using a method according to anyone of claims 1 to 23 or using a probe according to claim 24 or 25.

Respectfully submitted,

WELSH & KATZ, LTD.

By Gerald T. Shekleton Registration No. 27,466

Dated: October 19, 2000

Welsh & Katz, Ltd. 120 South Riverside Plaza 22nd Floor Chicago, Illinois 60606 Telephone: 312/655-1500

ABSTRACT

The invention relates to the detection, identification and diagnosis of bacteria in samples in general and in articular in clinical samples such as blood, urine, saliva, cerebrospinal fluid that are taken from patients that are possible infected with a, as yet, unknown, possible pathogenic bacterium, or during follow-up diagnostic testing to, for example, evaluate therapeutic measures that have been taken so far to threat the disease. The invention provides a method for detecting or identifying a bacterium suspected of being present in a sample comprising testing said sample by Gram-staining and testing said sample with a probe according to an in situ hybridization protocol selected on the basis of the outcome of said Gram-staining. The invention also provides probes for use in said method.

15

20

25

30

WO 99/54502

r/pits.

09/673779

PCT/NL99/00223

Title: METHOD FOR THE RAPID DETERMINATION OF BACTERIA

422 Rec'd PCT/PTO 1 9 OCT 2000

The invention relates to the detection, identification or determination of bacteria in samples in general and in particular in clinical samples such asblood, urine, saliva, cerebrospinial fluid, faeces, pus and tissue that are taken from patients that are possibly infected with a, as yet unknown, possibly pathogenic bacterium, or during follow-up diagnostic testing to for example evaluate therapeutic measures that have been taken so far to treat the disease.

Traditional methods to determine or identify bacteria in general start with a Gram-stain, which is well known in the art. Such a stain can be performed on a sample immediately after sampling or, when not enough bacteria are present, after a short period of culturing of the sample. In general, four types of bacteria are found after Gram-staining; Gram-negative rods and cocci and Gram-positive rods and cocci. However, such a Gram-stain can only in very exceptional cases provide the clinician with the knowledge required to provide accurate therapy.

Examples of Gram-negative rods in clinical samples are Enterobacter, Klebsiella, Salmonella, Escherichia, Proteus and Pseudomonas species, of Gram-negative cocci are Neisseria species. Gram-positive rods that may be found in clinical samples are Bacillus species, of Gram-positive cocci are Enterococcus, Streptoccus and Staphylococcus species. Some of these, such as Streptoccus and Staphylococcus can easily be further determined or distinguished from each other by their morphological characteristics. Streptococci (and Enterococci) are characterised by chain-like character of cocci that are linked to each other whereas Staphylococci accumulate in clumps. Most other species, such as Enterococcus and

15

30

35

Streptococcus species cannot be distinguished by morphology alone. However, such relatively rough taxonomic distinction on a genus level cannot be considered satisfactory for clinical purposes and consequently further identification is required to establish proper

further identification is required to establish proper medication. For example in the case of Staphylococcus, these bacteria need to be further distinguished based on their coagulase positive (S. aureus) or coagulase negative (S. haemolyticus and others) character because these two groups require different antibiotic therapy.

In general, the exact species involved is determined by culturing techniques. To fully determine the species of a bacterium present in a clinical sample the following steps are in general required:

- (1) Pre-culturing of the sample in order to amplify the number of bacteria to a level above the lower detection limits of step (2).
 - (2) Culturing on selective and non-selective media.

These traditional methods are time consuming. On

20 average, a regular diagnostic procedure takes at least a
few hours (minimally 2) of pre-culturing followed by
minimally 24 hours of culturing on selective and nonselective media. This implies that it takes at least 26
hours before the clinician obtains a diagnosis on which he

25 or she can select appropriate antibiotics or base other
further treatment.

This latency-period between the sampling of a patient and the final diagnosis in most cases is critical for the treatment and the speed-of-recovery of the patient. During this latency-period a patient is in general treated with broad-spectrum antibiotics. The antibiotic of choice is mainly determined by the "clinical eye" of the clinician.

By selecting a broad-spectrum antibiotic, such therapies are in general successful in the eradication of the pathogen but a serious side effect of this strategy is the fact that in most instances the normal microbial flora

is affected also. This side-effect heavily decreases the patients defence against microbial invaders from the environment. Especially the lowering of the colonisation threshold of the gastro-intestinal tract may cause severe overgrowth by e.g. yeasts and fungi. The resulting secondary infection, or super-infection, in septicaemic patients who already suffer from a decreased immunity often leads to life-threatening situations.

Apart from the serious danger to the patient's

health, wide-spectrum antibiotic therapy poses another 10 threat. The repeated exposure of indigenous bacteria to antibiotics enhances the emergence of resistance against such an antibiotic. Especially when a resistance-gene is encoded on a plasmid, other (potential pathogenic) bacterial species may become resistant after the uptake of 15 the plasmid. This latter scenario is considered to be a major problem in hospital epidemiology. It is therefor of paramount therapeutic and epidemiological importance to speed up the methodological procedures in the diagnosis of blood samples from for example septicaemic patients to be 20 able to select specific antibiotic therapy designed for the specific pathogen found, thereby refraining from using broad-spectrum antibiotics.

general specific when beforehand knowledge exists about the species involved, cannot be used with samples containing uncharacterised species, and do thus not fit the acute needs when speedy diagnosis is needed on uncharacterised patient material. In general, these methods are also too slow to meet the needs of the clinician in providing care to his or her patients. Most, for example, require isolation of nucleic acid, or amplification of nucleic acid, or both, before the actual testing can be performed. Also, in those cases where resistance of a pathogen to antibiotics has already occurred, it is of utmost importance to be able to rapidly

the transfer of the state of th

ile i

identify the pathogen and rapidly select the antibiotic against which the pathogen is not resistant. To do this, the micro-organism would again have to be cultured, to determine its resistance pattern, thereby again

In short, there is a need for fast and reliable diagnosis of bacteria, present in for example clinical samples that may replace or add to the currently used culturing techniques.

introducing a lag in diagnosis.

10

15

20

25

30

35

5

The invention provides a method for determining, detecting or identifying a bacterium suspected of being present in a sample comprising

- a) testing said sample by Gram-staining and
- b) testing said sample with a probe according to an in situ hybridisation protocol selected on the basis of the outcome of said Gram-staining.

Rapid techniques for detecting bacteria and other bacteria in general are known. For example, in situ hybridisation is a well known technique, however, in general it has only been applied in specialised laboratories as a tool to detect and quantify the relative abundance of bacteria that are difficult to culture using traditional methodology or as a tool to quantify for example growth kinetics of already known bacteria in culture.

In short, in in situ hybridisation, nucleic acid probes, labelled with a reporter molecule such as an enzyme or a fluorescing substance, are reacted with specific nucleic acid sequences found specifically and preferably solely in the bacteria under study, which for this purpose has been permeabilised to let the probe enter the organism. As a target sequence nucleic acids of different origins are employed. Most commonly used as a target for in situ hybridisation is the 16s ribosomal RNA molecule. Other target molecules which can be used are:

15

20

2.5

30

35

23S ribosomal RNA, mitochondrial RNA, messenger RNA and nuclear DNA.

In situ hybridisation has never been successfully applied for rapid detection of bacteria in clinical samples because the presently used in situ hybridisation techniques are too inaccurate and too slow to give an advantage over traditional culturing.

First of all, hybridisation requires permeabilisation of the pathogen, and until now no generally applicable permeabilisation protocols have been developed that allow sufficient but restricted lysis of many or all of a broad range of unidentified bacteria. In general, mild permeabilisation leaves many bacteria (such as Staphylococcus spec.) inaccessible for subsequent hybridisation with probes, whereas rigorous permeabilisation often fully lyses most bacteria, thereby foregoing the possibility to detect them all together.

In addition, current protocols are in general timeconsuming multi-step procedures; hybridisation often
requires minimally 24 hours, thereby giving no relief to
the needs of the clinician who is only helped with
accurate and speedy diagnosis. Furthermore, they mostly
require beforehand knowledge about the genus or even
species involved in order to select appropriate probes;
having such beforehand knowledge is clearly not the case
in the event of a patient having an unidentified
infection. Also, the present, already inappropriate
hybridisation techniques do not allow to gather
information on the response against antibiotics of the
bacterium involved.

The invention provides a fast and reliable method for diagnosis, detection and/or determination of bacteria which may be present in a sample. Such a sample may be of various origin, it is for instance possible to apply a method as provided by the invention to a sample obtained

15

20

25

30

35

he i

PCT/NL99/00223

from a (contaminated) bacterial culture, or drinking water or food suspected to be contaminated with a bacterium.

In a preferred embodiment the invention provides a method to detect or identify a bacterium suspected of being present in a clinical sample. Herein, the term "clinical sample" comprises a sample obtained or derived from an animal, preferably a mammal, more preferably a human being. Such a sample may be sampled or tested because a bacterial infection or disease is suspected.

Such a sample can be of various origin, such as blood, serum, white blood cells, cerebrospinal fluid, synovial fluid, tissue, biopsies, urine, saliva, faeces, and others. In a preferred embodiment the invention provides a method wherein said sample is mammalian blood, preferably being derived from a human.

A sample can be a primary sample or it can be a secondary or sub-sample which is derived from a primary sample by diluting, splitting or culturing it one or more times. Diluting allows determining the relative abundance of a bacterium in a sample, thereby thus providing a method allowing not only qualitative but also quantitative determination of a bacterium. A sample can be tested directly after it has been obtained or after it has been stored, for example by cooling or freezing and secondary or sub-samples can be tested in parallel or subsequent from each other.

The invention provides a method comprising determining by Gram-staining the Gram-positive or Gram-negative and rod or coccus type of bacterium in a clinical sample and further testing said sample according to an in situ hybridisation protocol selected on the basis of the outcome of said Gram-staining. A primary advantage of a method according to the invention is the speed with which analyses can now be performed. Total analysis time, when using a method according to the invention, is greatly reduced, when compared with existing in situ hybridisation

15

20

25

30

35

-

WO 99/54502

protocols. For example, Gram-positive Streptococci can now be determined from within about 30-60 minutes, Gram-negative rods from within about 45-90 minutes, if needed, whereas traditional protocols often need a working day or more. On top of that, often a first indication, or even a definitive selection, of a preferred antibiotic for therapy can be given, based on the results of the testing.

A preferred embodiment of the invention is a method for the detection or identification of bacteria in a clinical sample of blood of patients who are suspected to suffer from a septicaemia. In a preferred embodiment a method provided by the invention makes use of labeled probes, such as fluorescently labeled single strain DNA-, RNA- or PNA-probes, directed against specific target sequences on for example the ribosomal RNA of the target bacterium present in the sample.

The invention provides a method wherein classical Gram-staining indicates the presence of a Gram-negative or Gram-positive bacterium in said sample, further comprising determining the rod or coccus character of said bacterium, thereby establishing the subsequent testing protocol.

When a Gran-negative bacterium is of the rod type, the invention provides a method further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in Escherichia coli, in Klebsiella pneumoniae, in Klebsiella oxytoca, in Serratia marcescens, in Enterobacter aerogenes, in Enterobacter cloacae, in Proteus vulgaris, in Proteus mirabilis, in Salmonella typhi, in Pseudomonas aeruginosa.

Furthermore, the invention provides a method wherein said character is of the Gram-negative coccus type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme. Also, when said Gram-staining indicates the presence of a Gram-positive bacterium in said sample, said method is further

15

30

413

'a, #

June Wille

٦, إ M M

63

£.3 an is WO 99/54502

comprising determining the rod or coccus character of said bacterium, and when said Gram-positve character is of the rod type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme and/or Proteinase K.

In addition, when said character is of the Grampositive coccus type, a method is provided further comprising determining a chain-like or clump-like character of said bacteria before a hybridisation protocol is selected. When before mentioned character is chainlike, a method provided by the invention is further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme, and further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in Enterococcus faecalis, in Streptococcus pneumoniae, in Streptococcus mitis, in Streptococcus viridans, in Streptococcus sanguis, in Enterococcus faecium.

In addition, a method is provided wherein said character 20 is clump-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysostaphin and or Proteinase K, further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in 25 Staphylococcus aureus, in Staphylococcus haemolyticus, in Staphylococcus saprophyticus.

Probes used in a method as provided by the invention can be directed against various target nucleic acid molecules found in a bacterium which can be used are for example ribosomal RNA, mitochondrial RNA, plasmid DNA, messenger RNA and nuclear DNA. It is also possible to select as target molecules nucleic acid from the above discussed antibiotics resistance genes, which can be found in a plasmid or integrated in the bacterial genome.

15

20

25

In a preferred embodiment, a method provided by the invention uses as a target for in situ hybridisation a (16S) ribosomal RNA molecule. In a particular embodiment of the invention said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GTAGCCCTACTCGTAAGG or GAGCAAAGGTATTAACTTTACTCCC or GTTAGCCGTCCCTTTCTGG.or TTATCCCCCTCTGATGGG or AGAGAAGCAAGCTTCTCGTCCG or CCGAAGGGGAAGGCTCTA or AGAGAAGCAAGCTTCTCGTCCGTT, each selected in relation to a method as provided by the invention or in relation to congruent antibiotic sensitivity of a bacterium recognised by said probe.

In addition, a method is provided by the invention that is further comprising hybridising said sample with at least one positive control probe capable of hybridising with nucleic acid found in a majority of bacterial species and/or with at least one negative control probe not being capable of hybridising with nucleic acid found in a majority of bacterial species. Preferably said majority comprises at least 90% of bacterial species, especially with those species found in general with possibly infected (septicaemic) patients. A method as provided by the invention is even more specific and/or sensitive when at least 95%, preferably at least 99% of said species is reactive with said positive control probe or no more than 5%, preferably no more than 1% is reactive with said negative control probe.

Such a positive or negative control probe as provided by the invention is given in the experimental part, in general said positive control probe comprises no more than five mismatches with a probe with the sequence GCTGCCTCCCGTAGGAGT and/or said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGGCAGC.

20

25

30

35

Ľ, gji ħ, į

Furthermore, the invention provides a method with additional value to the clinician in that in said method a probe is selected for its reactivity with one or a group of bacterial genera and/or (sub) species having congruent susceptibility to antibiotic treatment. Such a probe detecting or identifying a bacterium in a sample, preferably a clinical sample, is capable of hybridising with nucleic acid found in a group of bacterial general and/or species or subspecies such as found with Staphylococcus and many other bacteria having congruent susceptibility to antibiotic treatment.

In a preferred embodiment of the invention, such a probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GAGCAAAGGTATTAACTTTACTCCC (i.e. reactive with bacteria for which amoxycillin treatment is most likely effective) or GTAGCCCTACTCGTAAGG (cephalosporin treatment) or GTTAGCCGTCCCTTTCTGG (piperacillin and/or aminoglycoside) or TTATCCCCCTCTGATGGG or GCCACTCCTCTTTTCCGG (amoxycillin) or GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGGCTCTA (vancomycin) or AGAGAAGCAAGCTTCTCGTCCGTT or AGAGAAGCAAGCTTCTCGTCCG (flucloxacillin).

In a much preferred embodiment of the invention a one-step procedure is used for both binding target bacteria (in the sample) to a microscopic slide and fixing intracellular structures. In the experimental part, various lysis buffers and fixating technique are provided that utilise such a one-step procedure.

Furthermore, the invention provides a diagnostic test kit comprising means for detecting or identifying a bacterium suspected of being present in a sample using a method according to the invention or using a probe according to the invention. Such a diagnostic kit for example at least comprises probes or a set of probes specific for the detection of pathogenic bacteria.

labels are also known.

WO 99/54502

10

15

20

30

35

Instructions for a method comprising in situ hybridisation may be added. Optionally, said probes, which can be common nucleic acid or peptide nucleic acid probes, are linked to reporter molecules such as direct fluorescent labels. Other reporter molecules, such as enzymes or radioactive

In addition, said kit may comprise one or more of the necessary buffer solutions, such as lysis buffer or hybridisation, optionally in ready made form, or for example cover slips and reaction vials. Said kit may fully comprise sets of probes reactive with a wide gamut of (pathogenic) bacteria, optionally characterised by reactivity with bacteria of congruent antibiotic susceptibility, or may comprise sets of probes specifically directed against bacteria of Gram-positive of -negative, rod, coccus or chain- or clump-like character.

Such a kit may also comprise probes specifically reactive with antibiotic resistance genes, providing a positive identification of least applicable antibiotic treatment.

The invention is further explained in the experimental part of the description which is not limiting the invention.

25 Experimental part

An example of a set of probes specific for the detection of pathogenic bacteria and an example of a new protocol for high-speed in situ hybridisation are presented. The methodology described here is for example used for both a preliminary screening of samples from septicaemic patients or as a full substitute on the basis of which therapeutic decisions are made. The invention thus provides a rapid and reliable method for determining the species and/or the genus of a bacterium present in a blood sample collected from a septicaemic patient.

25

30

Components

A set of fluorescently labeled oligonucleotide probes designed to hybridise specifically with a group of pathogenic bacteria (i.e. genus-specific probe) or with one specific pathogen (i.e. species-specific probe) or with bacteria with congruent susceptiblity or resistance to antibiotics.

A protocol for fast in situ hybridization of bacteria present in samples of blood collected from septicaemic patients, using the said probes.

Oligonucleotide probes designed to hybridize specifically with a group of pathogenic bacteria.

In a particular embodiment of the invention a method provided by the invention is exemplified by making use of 16S rRNA target molecule because a large databank containing 16S rRNA-sequences exists and is freely accessible via the Internet. Labeled probes form an essential part in in situ hybridizations. The present invention provides a set of probes which have been designed in an unexpected novel manner i.e. not based on normal taxonomic principles but rather on their pathological significance. The group of probes which apply to this particular embodiment of the invention have been designed in such a way that they span group(s) of bacteria which are clustered on the basis of presumed congruent sensitivity to antimicrobial agents. Positive identification thus yields direct therapeutic information. Grouping bacteria on the basis of their presumed antibiotic susceptibility results in groups of bacteria containing one to several hundreds of different species.

PCT/NL99/00223

on the criteria of presumed antibiotic susceptibility patterns is much faster over classical culturing methods that still suffer from fenotypic variability induced by environmental factors. The probes are preferably labelled with enzymatic or fluorescent labels. Current fluorescent labels which are applicable in this invention are:

- 1) Direct fluorescent labels:
- Fluorescein-isothiocyanate (FITC)
- 10 Tetramethylrhodamine-5-isothiocyanate (TRITC)
 - Texasred
 - 5(6)-carboxyfluorescein-N-hydroxysuccimide-ester (FLUOS[™])
 - 7-amino-4-methylcoumarin-3-acetic acid (AMCA")
- 15 Phycoerythrin
 - Indocarbocyanine dyes such as Cy3, Cy5 and C7
 - Any other direct fluorescent label
 - 2) Indirect fluorescent labels:
 - Enzymes such as alkaline phosphatase or
- horseradishperoxidase either attached directly or via a C6-thiol linker and used in combination with chemiluminescent substrates like AMPPD (3-('spiroadmantane)-4-methoxy-4-(3'-phosphoryloxy)-phenyl-1,2-dioxethane) or fluorescence generating substrates.
- 25 Digoxigenin (DIG) in combination with anti-DIG antibodies labeled with:
 - gold particles
 - fluorescent labels
- Enzymes such as alkaline phosphatase or horseradish peroxidase, optionally in combination with chemiluminescent substrates like AMPPD (3-('spiroadmantane)-4-methoxy-4-(3'-phospho-ryloxy)-phenyl-1,2-dioxethane) or fluorescence generating substrates.
- Biotin in combination with streptavidin or avidin and labeled just like the anti-DIG antibodies

William of the state of the sta

1.

إربا

4.1

Mariji mang apang again dinan dinan Salah James Sandi yang Again

PCT/NL99/00223

Dinitrophenyl as hapten in combination with appropriate antibodies and labeled just like the anti-DIG antibodies

Any other indirect fluorescent or enzymatic label

5

10

15

Fluorescent labels allow direct microscopic analysis preferably combined with image analysis. For the detection of fluorescent oligonucleotide probes hybridised to ribosomal RNA of the target bacterium, photography can be applied. However quantitation by this method is hampered by the absence of objective criteria by means of which discrimination between hybridized and non-hybridized cells can be performed. Therefore for objective evaluation of probe-specificity, an image analysis system is employed which allows fluorimetrical reading of individual bacterial cells.

A protocol for fast in situ hybridization of bacteria present in samples of blood

20

25

30

35

Protocols for the detection of rRNA in situ typically utilise both a lytic reagent for permeabilisation of the bacterial cell wall and fixatives to preserve structural and molecular integrity of cellular components. However, the results of such hybridizations are highly dependent on the type, concentration and incubation-time of both the lytic reagent and the fixative. Component 2 of the invention consists of a protocol for in situ hybridization in which both permeabilization and fixation have been optimized for a subsequent hybridization of maximally 2 hours. For this protocol it was important to ensure that the hybridization procedure used was applicable to a wide variety of unidentified bacteria. Differentiated use of

lytic reagents could only be based on information obtained from direct Gram-staining of the (pre-cultured) blood

sample. After extensive validation the novel protocol had the following unique characteristics:

20

25

30

35

A optimal lytic reagent can be chosen on the basis of the gram-stain of the pathogen present in the sample of blood. This procedure of differentiated permeabilisation is novel to regular protocols for in situ hybridisation in which the permeabilisation is always dedicated to the permeabilisation of one or a defined group of target

A one-step procedure is used for both binding target bacteria (in the sample) to the microscopic slide and fixing intracellular structures. Procedures presented in the current scientific literature all use multi-step protocols for binding, fixing and dehydration of the bacterial cells in order to condition them for optimal hybridisation.

bacteria. In this new procedure a very wide array of unidentified bacteria can sufficiently be permeabilised

without destruction of intracellular structures.

The hybridisation time is shortened to 2 hours. Regular protocols for in situ hybridisation utilise a hybridisation time of minimally 24 hours, rendering them useless for rapid diagnostic applications.

The invention also provides kits for carrying out the rapid detection of bacteria in blood samples according to the invention. Such a kit will usually comprise at least a probe or probes and optionally other reagents such as components for hybridisation-fluid, washing-fluid and permeabilisation-fluid.

Such a kit may be applied in a routine bacteriology laboratory or in a bedside environment, both as a fast screening method or as a full substitute for classical identification methods.

Examples of probe design and development

The following probes for example were found to hybridise the most predominant species of pathogens which

WO 99/54502

are found in blood from septicaemic patients. In addition each probe hybridises with a species or a cluster of bacteria which share congruent (but often not identical) antibiotic sensitivity patterns

	ID Se	quence (5'-3')1	Region ²	Specificity ³
	y ec	TGCCTCCCGTAGGAGT	V2	Bacterial Kindom
	B AC	TCCTACGGGAGGCAGC	D.n	no matches
10	C GC	CTGCCAGTTTCGAATG	V2	Salmonella spp. Klebsiella spp.
				Enterobacter spp.
	D GT	AGCCCTACTCGTAAGG	٧7	K. oxytoca, S. marcescens,
				Enterobacter spp, Proteus spp
	e ga	GCAAAGGTATTAACTTTACTCCC	V3	E. Coli
15	F TT	ATCCCCCTCTGATGGG	v3	E. faecalis
	c cc	TAATGCAGCGCGGATCC	V2	aureus, 5. haemolyticus
	н сс	CAAGGGGAAGGCTCTA	V6	s aureus, S. saprophyticus
	I AG	agaagcaagcttctcgtccg	v1	Streptococcus spp.
	J G1	TAGCCGTCCCTTTCTGG	V3	P. acruginosa
20	K AG	Ingaagcaagcttctcgtccgtt	V2	S. aureus
	L GC	CACTCCTCTTTTCCGG	? ?	Enterococcus faecium

¹ Each probe optionally contains an FITC-label at the 5'-end

- ² The variable region on the 16S rRNA where the targetsequence of the probe is positioned.
 - ³ The species or genus which rRNA contains a match with the sequence of the probe.
- 30 Protocol example.

A newly devised protocol for fast in-situ hybridization of pathogens in blood from septicaemic patients. This version consists of a step-wise version which can directly be used in a laboratory environment.

- 35 1 Collect a sample of blood from a patient using a vacuum sealed culture bottle.
 - 2 Place the culture bottle in the pre-culturing machine (e.g. BactAlert, Organon Teknika, Durham, NC 27704) to monitor the growth of the pathogen. On-line
- 40 monitoring is performed by measuring the pH of the sample.

PCT/NL99/00223

- After bacterial growth in a sample of blood has been detected, perform a Gram-stain and take out the culture bottle and collect 1 ml. of blood from the bottle using a syringe.
- Using the syringe, put +/- 0.1 ml of this sample on a degreased glass slide. And streak out using a slide of glass.
 - 5 Dry the slide for 5 minutes on a hotplate (for example of approximately 50° C).
- 6 Fix during 5 min. in ethanol(96%):formaldehyde(37%) (9:1.)
 - 7 Dry the slide for 5 minutes on a hotplate. (Slides can be stored for several months if kept at room temperature in a dry chamber)
- 15 8 Permeabilise **Streptococci** 20 min at 25 C with lysozyme (1 g/l)
 - 9 Permeabilise **Staphylococci** 20 min at 25 C with Lysostaphin (100 units/ml)
- 10 Rinse the slide with (demineralised) water for 5 minutes
 - 11 Dry the slide for 5 minutes on a hotplate.
 - Pipet hybridisation buffer(+SDS)-probe mix ([probe]=10ng/μl). Cover with a coverslip.
 - 13 Hybridize 2 hours (for example at 48°C).
- 25 14 Rinse 5 min using hybridisation buffer(-SDS).
 - 15 Mount the slide with a coverslip.
 - 16 Evaluate the slide.

phosphate buffered saline

- 30 8 g/1 NaC1
 - 0.2 g/l KCl
 - 1.44 g/I Na2HPO4
 - $-0.24 \text{ g/1 KH}_2\text{PO}_4$
 - adjust to pH 7.4.

Hybridisation buffer (+SDS)

- 900 ml Milli-Q water
- 52.6 g NaCl
- 2.52 g Tris (hydroxymethyl)-aminomethane
- 5 adjust to pH 7.5
 - add 90 ml water.
 - sterilize 15 minutes
 - + 10 ml SDS (10%) stock
- 10 hybridisation buffer (-SDS)
 - 900 ml Milli-Q water
 - 52,6 g NaCl
 - 2,52 g Tris
 - adjust to pH 7.5
- 100 ml Milli-Q water 15
 - sterilize 15 minutes

hybridisation buffer-probe mix

- 10 ng/ul of lyophilized probe in hybridisation buffer

20

lysozyme buffer

- 1,2 g Tris (=100mM)
- -1,86 g EDTA (=50mM)
- add 100 ml of milli-Q
- 25 - adjust to pH 7.5
 - 0,05 to 0,2 g lysozyme

Lysostaphin buffer

- 1,2 g Tris (=100mM)
- 30 -1,86 g EDTA (=50mM)
 - add 100 ml of milli-Q
 - adjust to pH 7.5
 - 0.05 to 0.2 g lysostaphin
 - dilute a lysostaphin stock (1000 ug/ml in milli-Q,
- stored at -20°C) 5-20 times in the above mentioned buffer.

Optionally, to lyozyme buffer or lyostaphin buffer 0,05 to 0,2 mg/ml Proteinase K is added.

- 5 ethanol-formaldehyde (90:10)
 - 1 ml formaldehyde 37%
 - 9 ml ethanol 96%

Validation of probe specificity

- Specificity of probes was tested against the complete RDA-database (http://rdpwww.life.uiuc.edu:80/rdphome.html) of 15 august 1996 using the CheckProbe command and was considered sufficient if a no more than five, preferably no more than two mismatches were observed. Furthermore, to
- determine whether the probes could reach their specific target sequence, a reference collection of 20 of the most predominant bacteria in sepsis were hybridised using both the protocol and the probes mentioned here above. The result of this validation is listed in table 2. As can be
- 20 read from this table all probes yield a satisfying hybridisation profile. Using the group-probes C and D it is possible to distinguish between: four groups of gramnegative rods:
 - C-positive and D-positive: Klebsiella oxytoca,
- 25 Enterobacter cloacae and Enterobacter aerogenes C-positive and D-negative: Klebsiella pneumoniae and Salmonella typhi
 - C-negative and D-positive: Serratia marcescens and Proteus vulgaris
- 30 C-negative and D-negative: Proteus mirabilis.

 For Escherichia coli and Pseudomonas aeruginosa two

 species-specific probes (E and J) have been designed and

 validated. These probes are optionally included because

 both Escherichia and Pseudomonas are notorious pathogens
- 35 which demand specific antimicrobial therapy. Probe F is a species-specific probe for Enterococcus faecalis, a

probes G and H.

PCT/NL99/00223

notorious pathogen. Probe I is a genus-specific probe which can be used in conjunction with probe F because Streptococci and Enterococci share the same morphology, while they require different antimicrobial treatment.

Using both probes G and H, 4 separate species of Staphylococci can be distinguished: G-positive and H-positive: Staphylococcus aureus G-positive and H-negative: Staphylococcus haemolyticus G-negative and H-positive: Staphylococcus saprophyticus G-negative and H-negative: Staphylococcus epidermidis 10 Probe K is a species-specific-probe for Staphylococcus aureus and can be used to support the results obtained by

15

WO 99/54502

Table 2.

Bacterium	A		C	D	E	F	G	н	I	1	k
Escherichia coli								:	<u> </u>	 	
Klebsiella pneumoniae											 . .
Klebsiella oxytoca										ļ	
Serratia marcescens										 	
Enterobacter aerogenes							\Box			 	
Enterobacter cloacae										 -	
Proteus vulgaris				10			1				†
Proteus mirabilis							-		-	 	
Salmonella typhi										 	
Pseudomonas aeruginosa											
Enterococcus faecalis				ſ ~~							
Enterococcus faecium											
Streptococcus pneumoniae				_							
Streptococcus mitis											
Streptococcus viridans											
Streptococcus sanguis										_	
Staphylococcus haemolyticus											
Staphylococcus aureus											
Staphylococcus epidermidis										-	
Staphylococcus saprophyticus		<u> </u>									

Legend: Probecoding see table 1, gray=positive

hybridization, white=no hybridization

Testing a method in whole-blood samples.

Preliminary testing of a new method in 50 whole blood samples which were found positive upon pre-culturing yielded a correlation of 96% between a method described here and the classical culturing method which was also applied to each of the 50 samples.

However, the results of a method described here could be obtained within 3 hours while culturing results took a mean analysis-time of 32 hours.

15

20

5

10

Anna agala.

A. in

W.

Man april 18

Brita mag

Further practical application

Septicemia is a pathological condition in which viable and multiplying bacteria may be present in the bloodstream.

This condition may occur after trauma or surgery (especially of the visceral organs), immunosuppression and obstetrical complications. It is a potential life—threatening condition and appropriate information on the causative agent should be available to the clinician as soon as possible. Bacteriological analysis of bloodsamples

WO 99/54502 PCT/NL99/00223 is routinely carried out by selective culturing of blood, which has previously been incubated on a general medium in a blood culture system. Currently, three continuousreading, automated and computed blood culture systems are available in clinical microbiology today: the BacTec 9240 (Becton Dickinson Instruments), the BacT/Alert (BTA, Organon Teknika) and the Extra Sensing Power (Difco Laboratories). All of these machines measure the production-rate of a bacterium specific metabolite in the culture-bottle containing the patient's blood supplemented with general nutrient broth. Subsequently if bacterial metabolic activity is detected, the positive blood culture sample is plated on appropriate selective media for further analysis. Microbial identification, taking the positive blood culture as a starting point, takes 24 h to 72 h to complete. Reduction of the analysis time may result in reduction of the use of broad-spectrum antibiotics as the genus or species of a pathogen gives an indirect indication of the most appropriate antibiotic. Subsequently, this may result in a lower frequency of 20 emergence of resistance against broad-spectrum antibiotics. Furthermore, it may result in lower cost because suppressive empiric therapy may be substituted by tailored and less expensive antibiotics with a smaller spectrum. Several methods for rapid detection of pathogens 25 in human blood have been described previously, most of them using the polymerase chain reaction or fluorescently labeled probes. Although these methods are fast and accurate, routine bacteriological analysis still heavily relies on classical culturing technique. It was therefore decided that for a molecular biological method to be successfully implemented in routine bacteriology it should be fast (maximally 1-4 h) and very easy-to-use (e.g. as complex as the preparation of a Gram-stained slide). A

simple and direct whole-cell hybridization assay using

species- and genus specific, fluorescently labeled

WO 99/54502

PCT/NL99/00223

oligonucleotide probes, was developed and validated. The probes described in this further practical application section comprise of single strain oligonucleotides labelled with fluorescein iso-thiocyanate at the 5'end; complementary to a genus- or species-specific sequence on the 16S- or the 23S ribosomal RNA of the target-organism.

Materials and methods

Blood samples 10

During the time of this study a total of 182 blood samples which tested positive in the BactAlert-blood culture machine were processed simultaneously, using both wholecell hybridization and accepted culturing methods.

Culturing

Microorganisms cultivated from positive blood cultures were identified by using the API-testsystem (BioMerieux, 20 France) or by using standard microbiological methods.

Probes

25 The characteristics of the probes used in this study are listed in Table 3. All probes consist of a single stranded oligonucleotide sequence covalently linked with fluorescein iso-thiocyanate at the 5'-end. Probes were synthesized by EuroGentee BV (Maastricht, The Netherlands)

15

ųij. EIS. ٦. إ

-

The state of the s

1

10

15

WO 99/54502

Table 3. Oligonucleotide probes used for hybridization of some pathogens normally detected in blood from septic patients

Probe*	Sequence (5'>3')	Target(s)	Preferred antibiotic**
EUB	GCTGCCTCCCGTAGGAGT	Bacterial Kingdom	n.a.***
non-EUB	ACTCCTACGGGAGGCAGC	negative control	n.a.
STREP	GTTAGCCGTCCCTTTCTGG	Streptococcus spp.	Penicilin G
EFAEC	TTATCCCCCTCTGATGGG	Enterococcus faecalis	Amoxycillin
EFAEM	GCCACTCCTCTTTTCCGG	Enterococcus faecium	Vancomycin
STAUR	AGAGAAGCAAGCTTCTCGTCCG	Staphylococcus aureus	Flucloxacillin
CNS	CGACGGCTAGCTCCAAATGGTTACT	Coagulase-negative Staphylococci	Vancomycin
ECOLI	GCAAAGGTATTAACTTTACTCCC	Escherichia coli	Amoxycillin
PSEUDAER	GGACGTTATCCCCCACTAT	Pseudomonas aeruginosa	Piperacillin+
ENTBAC	CATGAATCACAAAGTGGTAAGCGCC	Enterobacterium spp	aminoglycoside 2 nd generation cephalosporin

All probes consist of single strain DNA covalently linked with flurorescein iso-thyocyanate at the 5'-end. The E. coli-specific probe is directed against 235 rRNA, the other probes are directed against the 165 rRNA. Probe-nomenclature consists of mnemonics instead of a formal nomenclature-system for reasons of convenience.

- The antibiotic of first choice
- not applicable

**** Limited choice from all available therapeutics. On the basis of the local epidemiological situations other therapeutics may prevail

Whole cell hybridization

After gramstaining a streak-out preparation of a positive blood culture, a choice was made on the subsequent permeabilization-protocol and a set of appropriate probes (Table 3). Grampositive streptococci were permeabilized by incubating the fixed slide in a permeabilization-buffer (1 mg/ml lysozyme) during 5 min, gram-positive staphylococci were permeabilized by incubating the fixed slide in a second permeabilization-buffer (10 units/ml lysostaphin)

PCT/NL99/00223

during 20 min. Gram-negative rods were not permeabilized. Other gram-morphologies were not considered in this section because of the low incidence of these groups of bacteria in septicemia. From a positive blood culture fifteen µl was pipetted on a glass slide and subsequently streaked out. After air-drying the slide, the cells on the slide were fixed in a 4% formaldehyde-solution in pure ethanol. After permeabilization, the cells on the slide were hybridized at 50°C. Gram-negative rods were hybridized during 45 min, gram-positive staphylococci were hybridized during 2 h and gram-positive streptococci were hybridized during 5 min. Per gram-type a different set of probes was chosen (see Table 4).

WO 99/54502

Table 4 Performance of the method

Application-criterion*	Probe	Target organism	n**	T***
Each assay	EUB	All bacteria	182	1.00
	non-EUB	negative control	182	1.00
Gram-positive chains	STREP	Streptococcus spp.	20	1.00
	EFAEC	Enterococcus faecalis	10 =	1.00
	EFAEM	Enterococcus faecium	7	1.00
Gram-positive clumps	STAUR	Staphylococcus Aureus	13	1.,00
	CNS	Coagulase-negative	73	1.00
		Scaphylococci		
Gram-negative rods	ECOLI	Escherichia coli	23	1.00
	PSEUDAER	Pseudomonas aeruginosa	4	1.00
	ENTBAC	Enerobaccerium spp.	23	1.00

* The application criterion is the micromorphology of the pathogen in the initial gram-stain which is made after the BactAlert blood culture machine has detected microbolic activity in the bloodsample

** n=number of strains positively identified by culturing

*** r=correlation coefficient. This is the number of matching identifications between FISH and traditional culturing divided by the total number of assays

**** Comprises of 66% of the total number of samples tested. Other

samples showed no signal with the positive control probe

However, a probe (i.e. EUB-probe) positive for almost all bacteria and the reverse complementary probe (i.e. non-EUB probe) were included as a positive and negative control respectively, irrespective of the gram-type. Prior to use, probes were diluted to a concentration of 10 ng/ml in hybridization-buffer (20 mM Tris-HCl, 0.9M NaCl, 0.1% SDS, pH 7.2). After hybridization, the slides were rinsed during 10 min at 50°C in washing buffer (20 mM Tris-HCl, 0.9M NaCl, 0.1% SDS, pH 7.2) and mounted with VectaShield (Vector Laboratories, Burlinghame, USA). Immediately hereafter, the slides were evaluated using an epifluorescence microscope.

WO 99/54502 PCT/NL99/00223 The results of this section show that identification using whole-cell hybridization dramatically increases the speed of the diagnosis. In Figure 1 a typical example of the microscopic image obtained after hybridizing a blood sample obtained from a patient suffering from Streptococcus pneumoniae sepsis using the STREP-probe is shown. Using the described protocol, a clear-cut positive signal was obtained. Repeated microscopic evaluation by . different observers confirmed the unambiguity of the interpretation of the images obtained by this method. In Table 4, the results of the study are listed. The observation that all strains hybridize positively with the EUB-probe indicates that the hybridization protocol is applicable for whole cell hybridization of the bacterial species and genera tested in this study. The negative 15 results obtained with the non-EUB probe indicate the absence of aspecific interaction between the probe and constituents of the cellular matrix. The speed of diagnosis (after the sample is positive in the BactAlert blood culture machine) varies between 25 min 20 (streptococci/enterococci) and 2 h (staphylococci), while routine bacteriological determination would take at least 24 h to 48 h. The advantage to the patient is obvious

because, as can be read from Table 3, the clinician is able to start appropriate antimicrobial therapy within the 25 working day instead of after 24 h to 48 h. Being able to choose the most appropriate antibiotic also diminishes the need for broad-spectrum antibiotics therewith indirectly lowering the incidence of antibiotic-resistance. In table 4 the results obtained in this section are mentioned. 30

Broader application of the product

In its current form the product can be used for fast in situ detection of pathogenic bacteria in blood. However, 35 the product can also be used for detection of pathogens in

PCT/NL99/00223

WO 99/54502

other clinical samples. Experiments using the current product (i.e. probes and protocol) in another type of clinical sample have been carried out. The sample-types were: liquor and ascites. Results indicate that

- application of the product in these samples is perfectly well possible. Future application include:
 - New probes for other relevant species/genera
 - Other types of clinical samples like: sputum, pus,
- urine, where generally non-septicaemic bacteria, such as Legionella pneumoniae can be found, using a method according to the invention.

Advantages of whole-cell hybridization

15

30

Man and Beef,

7.

1,0

M GAR

Man and day offer

- Rapid diagnosis enabling the clinician to easily choose the appropriate antibiotic
- Less use of broad spectrum antibiotics, therewith lowering the incidence of antibiotic resistance
- 20 Cheap, a typical FISH-analysis is about 50% cheaper than a traditional culturing-based analysis.
 - ~ Easy to perform. A FISH-based analysis requires less actions and less hands-on time than a gram stain

25 Lay-out of kits

There are many possibilities for possible kit formats, several are listed below.

One main kit for 100 Tests (1 test is I positive control, I negative control and one unknown) consisting of all kits 1-4 listed below including a detailed protocol. Or the kits listed below alone or in a combination.

Ē,b

Kit 1 (the control kit):

WO 99/54502

- Lyophilized positive control probe (such as EUB or probe(s) functionally related thereto)
- 5 Lyophilized negative control probe (such as non-EUB or probe(s) functionally related thereto)
 - Lyophilized hybridization buffer (20 mM Tris-HCl, 0.9M NaCl, 0.1% SDS, pH 7.2)
- 10 Kit 2 for gram-negative samples:
 - Lyophilized probe such as ECOLI, PSEUDAER, ENTBAC or probe(s) functionally related thereto
- Lyophilized hybridization buffer (20 mM Tris-HCl, 0.9M NaCl, 0.1% SDS, pH 7.2)

Kit 3 for gram-positive streptococci-like bacteria:

- Lyophilized probes such as STREP, EFAEC, EFAEM or
 probe(s) functionally related thereto
 - Lyophilized hybridization buffer (20 mM Tris-HCl, 0.9M NaCL, 0.1% SDS, pH 7.2) with 1 mg/ml hen-eggwhite lysozyme.
- 25 Kit 4 for staphylococci-like bacteria:
 - Lyophilized probes such as STAUR, CNS or probe(s) functionally related thereto
- Lyophilized hybridization buffer (20 mM Tris-HCl, 0.9M
- 30 NaCl, 0.1% SDS, pH 7.2) with 10 units/ml lysostaphin

Basic labeling of probes is with fluorescein iso-thio cyanate. Alternatively kits may contain probes with other fluorescent labels e.g. Cy-3, CyberGreen, Phyco-erythrin

etc., or combinations therewith. Alternatively kits may contain a number of probes in one tube (Eppendorf cup)

WO 99/54502

The period and properties he was a few of the control of the contr

with different fluorescent labels for simultaneous detection of different targets with one test. We have successfully detected streptococci and enterococci in one sample in this way. In Fig 2 an example of this type of application is shown. Here, a mixed infection of morphologically indistinguishable gram-positive streptococcus-like bacteria are successfully hybridized with both the STREP-probe (FITC-label) and the EFAEC-probe (Cy3-label). Other combinations of the above kits may also be provided as one kit for a specific application.

High the supplementation of the supplementary of th

Legends

Figure 1: Cells of Streptococcus pneumoniae show intense bright fluorescence after 5 min. of incubation with the STREP-probe at 50°C. Magnification = 10x100, fluorochrome = fluorescein iso-thiocyanate

Figure 2: Mixed infection with E. faecalis and S. pneumoniae hybridized simultaneously with both the STREP10 probe (FITC-label) and the EFAECAL-probe (Cy3-label). Also a fluorescent DNA/RNA stain (DAPI) has been applied to detect all nucleic acid.

09/673779

- 1. A method for determining a bacterium suspected of being present in a sample comprising 422 Rec'd PCT/PTO 1 9 OCT 2000 a) testing said sample by Gram-staining and
- b) testing said sample with a probe according to an in situ hybridisation protocol selected on the basis of the outcome of said Gram-staining.
- 2. A method according to claim 1 wherein said sample is a clinical sample.
- 3. A method according to claim 2 wherein said sample is mammalian blood, preferably being derived from a human.
- 4. A method according to claim 1, 2 or 3 wherein said Gram-staining indicates the presence of a Gram-negative bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.
- 5. A method according to claim 4 wherein said character is of the rod type, further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in Escherichia coli, in Klebsiella pneumoniae, in Klebsiella oxytoca, in Serratia marcescens, in Enterobacter aerogenes, in Enterobacter cloacae, in Proteus vulgaris, in Proteus mirabilis, in Salmonella typhi, in Pseudomonas aeruginosa.
- 6. A method according to claim 5 wherein said nucleic acid is ribosomal RNA.
- 7. A method according to claim 6 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GTAGCCCTACTCGTAAGG or GAGCAAAGGTATTAACTTTACTCCC or GTTAGCCGTCCCTTTCTGG.
- 8. A method according to claim 4 wherein said character is of the coccus type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.
- 9. A method according to claim 1, 2 or 3 wherein said Gram-staining indicates the presence of a Gram-positive

bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.

- 10. A method according to claim 9 wherein said character is of the rod type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme and/or Proteinase K.
- 11. A method according to claim 9 wherein said character is of the coccus type, further comprising determining a chain-like or clump-like character of said bacteria.
- 12. A method according to claim 11 wherein said character is chain-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.
- 13. A method according to claim 12 further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in Enterococcus faecalis, in Streptococcus pneumoniae, in Streptococcus mitis, in Streptococcus viridans, in Streptococcus sanguls, in Enterococcus faecium.
- 14. A method according to claim 13 wherein said nucleic acid is ribosomal RNA.
- 15. A method according to claim 14 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence TTATCCCCCTCTGATGGG or AGAGAAGCAAGCTTCTCTGTCCGG.
- 16. A method according to claim 11 wherein said character is clump-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysostaphin and/or Proteinase K.
- 17. A method according to claim 16 further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in Staphylococcus aureus, in Staphylococcus haemolyticus, in Staphylococcus saprophyticus.
- 18. A method according to claim 17 wherein said nucleic acid is ribosomal RNA.

- 19. A method according to claim 18 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCTAATGCAGCGCGGATCC or CCGAAGGGAAGGCTCTA or AGAGAAGCAAGCTTCTCGTCCGTT.
- 20. A method according to any of claims 4 to 19 further comprising hybridising said sample with at least one positive control probe and/or with at least one negative control probe.
- 21. A method according to claim 20 wherein said positive control probe comprises no more than five mismatches with a probe with the sequence GCTGCCTCCCGTAGGAGT and/or wherein said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGCAGC.
- 22. A method according to anyone of claims 1 to 21 further comprising a one-step procedure to bind bacteria present in said sample to a microscopic slide and simultaneously fix intracellular structures.
- 23. A method according to anyone of claims 1 to 22 wherein said probe is selected for its reactivity with one or a group of bacterial genera and/or species having congruent susceptibility to antibiotic treatment.
- 24. A probe detecting or identifying a bacterium in a sample, preferably a clinical sample, said probe designed to hybridise specifically with nucleic acid in bacteria with congruent susceptibility or resistance to antibiotics.
- 25. A probe according to claim 24 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GTAGCCGTACTCGTAAGG or GAGCAAAGGTATTAACTTTACTCCC or GTTAGCCGTCCCTTTCTGG or TTATCCCCCTCTGATGGG or AGAGAAGCAAGCTTCTCGTCCG or GCCACTCCTCTTTTCCGG or GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGGCTCTA or AGAGAAGCAAGCTTCTCGTCCGTT.

26. A diagnostic test kit comprising means for detecting or identifying a bacterium suspected of being present in a sample using a method according to anyone of claims 1 to 23 or using a probe according to claim 24 or 25.

WO 99/54502

09/673779

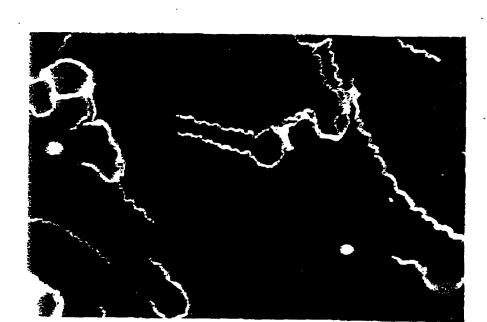


Figure 1: Streptococci in blood (10x100)



Figure 2: Mixed culture of E, faecalis and E faecium (10x100)

Declaration and Power of Attorney Patent Application (Design or Utility)

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: "Method for the Rapid Determination of Bacteria".

the specification of which

	is attached hereto	
Χ	was filed on April 19, 1999 as application serial no. 09/673,779 and or PCT	
	International Application number PCT/NL99/00223 and was amended on	(if
	applicable).	`

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information know to me to be material to patentability as defined in 37 C.F.R.§1.56.

I hereby claim foreign-priority benefits under 35 U.S.C.§119(a)-(d) or 35 U.S.C.§365(b) of any foreign application(s) for patent or inventor's certificate, or 35 U.S.C.§365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate of PCT International application having a filing date before that of the application on which priority is claimed.

	Prior Foreign App	lication(s)
Number 98201253.6	Country EP	Day/Month/Year Filed 20 April 1998
Number	Country	Day/Month/Year Filed
Number	Country	Day/Month/Year Filed

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below:

Prior Provisional Application(s)			
Serial Number	Day/Month/Year Filing Date		
Serial Number	Day/Month/Year Filing Date		
Serial Number	Day/Month/Year Filing Date		

I hereby claim the benefit under 35 U.S.C. §120 of any United States application(s), or under 35 U.S.C. §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112, I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information known to me to be material to patentability as defined in 37 C.F.R.§1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

Prior U.S. or International Application(s)			
ed, pending, abandoned)			
ed, pending, abandoned)			
ed, pending, abandoned)			
_			

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C.§1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Power of Attorney

As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Attorney	Requisition Number
Donald L. Welsh A. Sidney Katz	16,665 24,003
Richard L. Wood	22,839
Jerold B. Schnayer Eric C. Cohen	<u> 28,903</u>
Joseph R. Marcus	27,429 25.060
Gerald S. Schur	22,053
Gerald T. Shekleton James E. Scheer	27,466
Daniel R. Cherry	29,434 29,054
Edward P. Gamson	29,381
Kathleen A. Rheintgen	34,044
Thomas W. Tolpin	27,600

I hereby authorize them or others whom they may appoint to act and rely on instructions from and communicate directly with the person/organization who/which first sends this case to them and by whom/which I hereby declare that I have consented after full disclosure to be represented unless/until I instructed otherwise.

Please direct all correspondence in this case to at the address indicated below:

WELSH & KATZ, LTD.

120 South Riverside Plaza, 22nd Floor
Chicago, Illinios 60606-3913

Full Name of Sole or First Inventor			
Family Name	First Given Name	Second Given Name	
<u>Jansen</u>	_Gijs <u>bert</u>	Johan	
	Residence and Citizenship		
City of Residence	State or Country of Residence	Country of Citizenship	
Giekerk_ \(\lambda \left[\left[\left] \)	The Netherlands	The Netherlands	
Post Office Address			
Street Address	City	State & Zip Code or Country	
Suderspaerlân 16	Giekerk	9061 BJ	
Signature of Inventor	XIV	Date 72-4-00	

D.

	Full Name of Second Inventor, if ar			
Family Name	First Given Name	Second Given Name		
<u>Deg</u> ener	John	-Edward ->		
,	Residence and Citizenship			
City of Residence	State or Country of Residence	Country of Citizenship		
Drachten NI	The Netherlands	The Netherlands		
Post Office Address				
Street Address	City	State & Zip Code or Country		
De Rozentuin 1	Drachten	9203 LP		
Signature of Inventor		Date 22-11-00		

First Given Name Gjalt	Second Given Name		
Cialt			
Glait	Wietze		
Residence and Citizenship			
State or Country of Residence	Country of Citizenship		
The Netherlands	The Netherlands		
Roderwolde The Netherlands The Netherlands Post Office Address			
City	State & Zip Code or Country		
Roderwolde	9315 PC		
ANATO P	Date 22-11-00		
	State or Country of Residence The Netherlands Post Office Address City		

200

The light of high of and of an of the high of the high